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Artificial intelligence algorithms for recurrence risk score prediction in early-stage breast cancer: A multicenter study of 437 cases.

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Background: In non-developed and developing countries, the 21 gene assay (Oncotype DX) test is expensive and not covered by private and social health insurance, which limits its use. However, clinicians need this test for treatment prediction in early stage breast cancer. Therefore, we aimed to predict the risk of recurrence in patients using artificial intelligence (AI) algorithms. **Methods:** This study was conducted with 437 early-stage breast cancer patients whose recurrence risk scores were determined by 21 Oncotype DX and were followed in 14 oncology centers in Turkey between 2012 and 2022. The optimum cut-off for the 21 gene assay risk score (RS) was found by ROC analysis using the patients' recurrence information (scale of RS ≥17: high risk, <17: low risk). In artificial intelligence prediction models, patients with a 21 gene assay risk score ≥17 were considered high risk. Additionally, algorithm predictions were made within other cut-offs recommended in the literature (<10, 11-25, >25). Python programming language was used in the analyses. The Random Forest (RF), Logistic regression (LG) and K-Nearest Neighbors (KNN) were used as AI prediction algorithms. **Results:** The study analyzed 437 women with an average age of 49.49±10.30. During the follow-up period from 2012 to 2022, 7.1% of the patients experienced a recurrence. AI prediction algorithms which were RF, LG, and KNN generated confusion matrices for two classes, with a threshold of 17 and 25. The algorithms were then applied to the dataset with risk score thresholds of 1-10, 11-25, and greater than 25, resulting in three classes. The dataset was analyzed using recall, precision, and F1 score values. The results showed that RF had the most accurate predictions for RS = 17 (Table). **Conclusions:** The use of artificial intelligence algorithms in predicting the risk of recurrence in early stage breast cancer is promising in determining treatment decisions for clinicians who cannot access genetic results. Research Sponsor: None.

Accuracy of the AI algorithms on the oncotype DX dataset.

		Precision			Recall			F1 score		
Cut-off		**RF**	**LG**	**KNN**	**RF**	**LG**	**KNN**	**RF**	**LG**	**KNN**
17	<17	1.00	0.84	0.76	1.00	0.90	0.80	1.00	0.87	0.78
	≥17	1.00	0.88	0.77	1.00	0.81	0.73	1.00	0.84	0.75
25	>25	1.00	0.87	0.89	1.00	1.00	0.95	1.00	0.93	0.92
	>25	1.00	1.00	0.76	1.00	0.46	0.57	1.00	0.63	0.65
3 Classes	1-10	0.40	0.33	0.29	0.09	0.04	0.09	0.14	0.08	0.13
	11-25	0.71	0.71	0.64	0.94	0.90	0.89	0.81	0.79	0.74
	25>	0.91	0,72	0.53	0.70	0.70	0.27	0.79	0.71	0.36

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